

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: December 13, 2004, 21:15:51 ; Search time 31 Seconds  
(without alignments)  
2731.315 Million cell updates/sec

Title: US-09-976-054-5  
Perfect score: 588  
Sequence: 1 cgtccgcgcgcgcgcgacttc.....ggaatnntagataaaaaant 440

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_n2p.model -DEV=xlp

Q=/cgn2\_1/USPTO\_spool\_p/US09976054/runat\_13122004\_160520\_24790/app\_query.fasta\_1  
.583

-DB=PIR\_79 -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09976054 @CGN\_1\_1\_63 @runat\_13122004\_160520\_24790 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%		Query	Length	DB	ID	Description
	No.	Score	Match				
	1	169.5	28.8	183	1	S20867	adenine phosphorib
	2	169	28.7	223	2	G86399	protein F17L21.24
	3	157.5	26.8	181	2	T06263	adenine phosphorib
	4	156.5	26.6	182	2	T07636	adenine phosphorib
	5	153.5	26.1	183	2	T05451	adenine phosphorib
	6	129.5	22.0	192	1	S71272	adenine phosphorib
	7	116	19.7	183	2	AF0562	adenine phosphorib
	8	115	19.6	183	1	RTECA	adenine phosphorib
	9	111	18.9	181	2	G82246	adenine phosphorib
	10	110	18.7	183	2	B90694	adenine phosphorib
	11	110	18.7	183	2	F85544	adenine phosphorib
	12	100	17.0	187	2	AD0379	adenine phosphorib
	13	98	16.7	180	2	G64111	adenine phosphorib
	14	94.5	16.1	182	2	F83453	adenine phosphorib
	15	84.5	14.4	180	1	RTMSA	adenine phosphorib
	16	84.5	14.4	188	2	T38223	probable adenine p
	17	84	14.3	180	2	AC2851	adenine phosphorib
	18	84	14.3	182	2	F81366	adenine phosphorib
	19	84	14.3	198	2	A97628	adenine phosphorib
	20	80.5	13.7	180	2	S36334	adenine phosphorib
	21	77	13.1	172	2	S75440	adenine phosphorib
	22	76.5	13.0	173	2	G82883	adenine phosphorib
	23	76.5	13.0	180	1	RTHUA	adenine phosphorib
	24	76	12.9	79	2	A87553	hypothetical prote
	25	75.5	12.8	307	2	D83295	transaldolase PA27
	26	74	12.6	172	2	AF2378	adenine phosphorib
	27	74	12.6	186	2	AF3311	adenine phosphorib
c	28	73.5	11.8	550	2	T36746	probable serine/th
c	29	73	11.7	306	2	T06435	ribonuclease S5 ho
c	30	73	11.7	891	2	G84693	probable proline-r
	31	71.5	12.2	182	2	B49927	adenine phosphorib
	32	71	12.1	183	1	A29596	adenine phosphorib
	33	71	12.1	184	2	S34831	adenine phosphorib
	34	71	12.1	219	2	B84326	hypothetical prote
	35	70.5	12.0	264	2	JC6125	U2 small nuclear r
	36	70	11.9	163	2	D83850	inorganic pyrophos
c	37	69.5	11.2	200	2	T52627	splicing factor RS
c	38	69.5	11.2	200	2	T05112	splicing factor 9G
	39	68.5	11.6	503	2	F95988	probable ATP-depen
	40	67	11.4	158	2	T42700	hypothetical prote
c	41	66.5	10.7	198	2	A45067	laminin B1 chain v
c	42	66.5	10.7	287	2	E83398	hypothetical prote
c	43	66.5	10.7	431	2	S09824	hypothetical prote
c	44	66.5	10.7	1415	1	EDBEGA	immediate-early pr
c	45	66	10.6	649	2	JQ0103	hypothetical 70K p

#### ALIGNMENTS

RESULT 1

S20867

adenine phosphoribosyltransferase (EC 2.4.2.7) 1 [similarity] - Arabidopsis  
thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
 C;Accession: S20867  
 R;Moffatt, B.A.; McWhinnie, E.A.; Burkhart, W.E.; Pasternak, J.J.; Rothstein, S.J.  
 Plant Mol. Biol. 18, 653-662, 1992  
 A;Title: A complete cDNA for adenine phosphoribosyltransferase from Arabidopsis thaliana.  
 A;Reference number: S20867; MUID:92216042; PMID:1558943  
 A;Accession: S20867  
 A;Molecule type: mRNA  
 A;Residues: 1-183 <MOF>  
 A;Cross-references: UNIPROT:P31166; EMBL:X58640; NID:g16163; PIDN:CAA41497.1; PID:g16164  
 A;Experimental source: strain cv.columbia  
 A;Note: the authors translated the codon CTC for residue 138 as Ser  
 A;Note: part of this sequence was confirmed by protein sequencing  
 C;Genetics:  
 A;Gene: apt; apt1  
 C;Function:  
 A;Pathway: purine salvage  
 C;Superfamily: adenine phosphoribosyltransferase  
 C;Keywords: glycosyltransferase; pentosyltransferase; salvage pathway

# Alignment Scores:

Pred. No.:	8.41e-13	Length:	183
Score:	169.50	Matches:	42
Percent Similarity:	54.26%	Conservative:	9
Best Local Similarity:	44.68%	Mismatches:	41
Query Match:	28.83%	Indels:	2
DB:	1	Gaps:	1

US-09-976-054-5 (1-440) x S20867 (1-183)

Qy	115	GATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAGCCA	174
Db	8	AspProArgIleAlaLysIleAlaSerSerIleArgValIleProAspPheProLysPro	27
Qy	175	GGGATNATGTTTTAGGACATCANGANGNTGNTGTTCGATCCCAAGGCGNTCCGTGACAAC	234
Db	28	GlyIleMetPheGlnAspIleThrThrLeuLeuLeuAspThrGluAlaPheLysAspThr	47
Qy	235	ATATACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCACNTGGAAANTAGGAGTTAA	294
Db	48	IleAlaLeuPheValAspArgTyrLysAspLysGlyIleSerVal-ValAlaGlyValG1	67
Qy	295	AGCTAGAGGGNTCANTTTTCGGAACAACACTANNTCTTANAANNAATTGGTCAAAAATNGGTG	354
Db	67	uAlaArgGlyPheIlePheGlyProProIleAlaLeuAlaIleGlyAlaLys---PheVa	86
Qy	355	NCNATTGAGGAAGCNAATNAGNTGCCANGCNAATGATT	394
Db	86	lProMetArgLysProLysLysLeuProGlyLysValIle	99

RESULT 2

G86399

protein F17L21.24 [imported] - Arabidopsis thaliana



## T06263

Alignment Scores:

US-09-976-054-5 (1-440) x T06263 (1-181)

## RESULT 4

T07636





C;Accession: S71272  
 R;Schnorr, K.M.; Laloue, M.; Hirel, B.  
 submitted to the EMBL Data Library, March 1996  
 A;Description: Isolation of cDNAs encoding two purine biosynthetic enzymes of  
 soybean and expression of the corresponding transcripts in roots and root  
 nodules.  
 A;Reference number: S71272  
 A;Accession: S71272  
 A;Molecule type: mRNA  
 A;Residues: 1-192 <SCH>  
 A;Cross-references: UNIPROT:Q42563; EMBL:X96866; NID:g1402893; PIDN:CAA65609.1;  
 PID:g1321681  
 A;Experimental source: strain cv. columbia; isolate A19  
 C;Genetics:  
 A;Gene: apt2  
 A;Map position: 1  
 C;Function:  
 A;Pathway: purine salvage  
 C;Superfamily: adenine phosphoribosyltransferase  
 C;Keywords: glycosyltransferase; pentosyltransferase; salvage pathway

Alignment Scores:

Pred. No.:	8.36e-08	Length:	192
Score:	129.50	Matches:	37
Percent Similarity:	45.74%	Conservative:	6
Best Local Similarity:	39.36%	Mismatches:	49
Query Match:	22.02%	Indels:	2
DB:	1	Gaps:	1

US-09-976-054-5 (1-440) x S71272 (1-192)

Qy	115	GATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAGCCA	174
Db	11	AspProArgLeuLysAlaIleSerAspAlaIleArgValIleProHisPheProLysThr	30
Qy	175	GGGATNATGTTTCAGGACATCANGANGNTGNTGTTTCGATCCCAAGGCGNTCCGTGACAAC	234
		:::	
Db	31	GlyIleMetPheGlnAspIleThrThrLeuLeuLeuAspProValAlaPheLysHisVal	50
Qy	235	ATATACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCACCNCTGGAAANTAGGAGTTAA	294
		:::                  :::      :::	
Db	51	ValAspIlePheValAspArgTyrLysHisMetAsnIleSerLeu-ValAlaGlyValG1	70
Qy	295	AGCTAGAGGGNTCANTTTCGGAACAACCTANNTCTTANAANNAATTGGTCAAAAATNGGTG	354
		:              :::	
Db	70	uAlaArgGlyPheIlePheGlyProProIleAlaLeuAlaIleGlyAlaLys---PheVa	89
Qy	355	NCNATTGAGGAAGCNNAATNAGNTGCCANGCNAATGATT	394
		:::	
Db	89	lProLeuArgLysProGlyLysLeuProGlyArgValIle	102

RESULT 7

AF0562

adenine phosphoribosyltransferase [imported] - *Salmonella enterica* subsp.  
*enterica* serovar Typhi (strain CT18)

C;Species: *Salmonella enterica* subsp. *enterica* serovar Typhi

A;Note: this species has also been called *Salmonella typhi*



C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
 C;Accession: AF0562  
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; Mungall, K.L.; Bentley, S.D.; Holden, M.T.G.; Sebaihia, M.; Baker, S.; Basham, D.; Brooks, K.; Chillingworth, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, J.; Feltwell, T.; Hamlin, N.; Haque, A.; Hien, T.T.; Holroyd, S.; Jagels, K.; Krogh, A.; Larsen, T.S.; Leather, S.; Moule, S.; O'Gaora, P.  
 Nature 413, 848-852, 2001  
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.G.  
 A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Typhi CT18.  
 A;Reference number: AB0502; MUID:21534947; PMID:11677608  
 A;Accession: AF0562  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-183 <PAR>  
 A;Cross-references: GB:AL513382; PIDN:CAD04968.1; PID:g16501754; GSPDB:GN00176  
 C;Genetics:  
 A;Gene: STY0527  
 C;Superfamily: adenine phosphoribosyltransferase

Alignment Scores:

Pred. No.:	4.08e-06	Length:	183
Score:	116.00	Matches:	28
Percent Similarity:	52.78%	Conservative:	10
Best Local Similarity:	38.89%	Mismatches:	33
Query Match:	19.73%	Indels:	1
DB:	2	Gaps:	0

US-09-976-054-5 (1-440) x AF0562 (1-183)

```

Qy      103 ATGGCGTNCGCTGATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGAC 162
      |||          :::|||          :::   :::   |||          |||
Db      1  MetThrAlaThrAlaGlnGlnLeuGluPheLeuLysAsnSerIleLysSerIleGlnAsp 20

Qy      163 TTNCCAAAGCCAGGGATNATGTTTCAGGACATCANGANGNTGNTGTTTCGATCCCAAGGCG 222
      |||||          :::|||:::||||:::          |||||          |||||
Db      21  TyrProLysProGlyIleLeuPheArgAspValThrSerLeuLeuGluAspProLysAla 40

Qy      223 NTCCGTGACAACATATACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCACCNTGGAA 282
      :::|||          |||:::|||||||:::          |||||          |||||
Db      41  TyrAlaLeuSerIleGluLeuLeuValGluArgTyrLysAsnAlaGlyIleThrLys-Va 60

Qy      283 ANTAGGAGTTAAAGCTAGAGGGNTCANTTTTCGGA 316
      |||          :::|||||||          |||||          |||||
Db      60  lValGlyThrGluAlaArgGlyPheLeuPheGly 71

```

RESULT 8

RTECA

adenine phosphoribosyltransferase (EC 2.4.2.7) - *Escherichia coli* (strain K-12)

N;Alternate names: AMP pyrophosphorylase; transphosphoribosidase

C;Species: *Escherichia coli*

C;Date: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 09-Jul-2004

C;Accession: A25635; B25549; D64777

R;Hershey, H.V.; Taylor, M.W.

Gene 43, 287-293, 1986

A;Title: Nucleotide sequence and deduced amino acid sequence of Escherichia coli adenine phosphoribosyltransferase and comparison with other analogous enzymes.

A;Reference number: A91548; MUID:86301884; PMID:3527873

A;Accession: A25635

A;Molecule type: DNA

A;Residues: 1-183 <HER>

A;Cross-references: UNIPROT:P07672; GB:M14040; GB:M25902; NID:g145293;

PIDN:AAA23455.1; PID:g145294

R;Flower, A.M.; McHenry, C.S.

Nucleic Acids Res. 14, 8091-8101, 1986

A;Title: The adjacent dnaZ and dnaX genes of Escherichia coli are contained within one continuous open reading frame.

A;Reference number: A25549; MUID:87040775; PMID:3534795

A;Accession: B25549

A;Molecule type: DNA

A;Residues: 40-183 <FLO>

A;Cross-references: GB:X04487; NID:g43319; PIDN:CAA28173.1; PID:g809695

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.;

Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor,

J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: D64777

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-183 <BLAT>

A;Cross-references: GB:AE000153; GB:U00096; NID:g1786671; PIDN:AAC73571.1;

PID:g1786675; UWGP:b0469

A;Experimental source: strain K-12, substrain MG1655

C;Genetics:

A;Gene: apt

A;Map position: 11 min

C;Function:

A;Pathway: purine salvage

C;Superfamily: adenine phosphoribosyltransferase

C;Keywords: glycosyltransferase; homodimer; pentosyltransferase; salvage pathway

#### Alignment Scores:

Pred. No.:	5.44e-06	Length:	183
Score:	115.00	Matches:	28
Percent Similarity:	52.78%	Conservative:	10
Best Local Similarity:	38.89%	Mismatches:	33
Query Match:	19.56%	Indels:	1
DB:	1	Gaps:	0

US-09-976-054-5 (1-440) x RTECA (1-183)

Qy	103	ATGGCGTNCGCTGATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGAC	162
		::    :::	
Db	1	MetThrAlaThrAlaGlnGlnLeuGluTyrLeuLysAsnSerIleLysSerIleGlnAsp	20
Qy	163	TTNCCAAAGCCAGGGATNATGTTTCAGGACATCANGANGNTGNTGTTCGATCCCAAGGCG	222
		::   :: :: ::	
Db	21	TyrProLysProGlyIleLeuPheArgAspValThrSerLeuLeuGluAspProLysAla	40

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Qy      223 NTCCGTGACAACATATACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCACCNTGGAA 282
          :::|||      |||:::|||||||:::  |||||
Db      41 TyrAlaLeuSerIleAspLeuLeuValGluArgTyrLysAsnAlaGlyIleThrLys-Va 60

Qy      283 ANTAGGAGTTAAAGCTAGAGGGNTCANTTTCGGA 316
          |||  :::|||||||  |||||
Db      60 lValGlyThrGluAlaArgGlyPheLeuPheGly 71

```

# RESULT 9

G82246

adenine phosphoribosyltransferase VC1053 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)

C;Species: *Vibrio cholerae*

C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004

C;Accession: G82246

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, E.K.; Peterson, J.D.; Umayam, L.A.; Gill, S.R.; Nelson, K.E.; Read, T.D.; Tettelin, H.; Richardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.; McDonald, L.; Utterback, T.; Fleishmann, R.D.; Nierman, W.C.; White, O.; Salzberg, S.L.; Smith, H.O.; Colwell, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: G82246

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-181 <HEI>

A;Cross-references: UNIPROT:Q9KT52; GB:AE004187; GB:AE003852; NID:g9655516;

PIDN:AAF94212.1; GSPDB:GN00126; TIGR:VC1053

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC1053

A;Map position: 1

C;Superfamily: adenine phosphoribosyltransferase

## Alignment Scores:

Pred. No.:	1.72e-05	Length:	181
Score:	111.00	Matches:	26
Percent Similarity:	53.85%	Conservative:	9
Best Local Similarity:	40.00%	Mismatches:	29
Query Match:	18.88%	Indels:	1
DB:	2	Gaps:	0

US-09-976-054-5 (1-440) x G82246 (1-181)

```

Qy      124 TTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAGCCAGGGATNATG 183
          |||:::  |||  |||  |||  |||||  |||||  |||  :::
Db      6  LeuSerLeuIleLysSerSerIleLysSerIleProAspTyrProLysLysGlyIleLeu 25

Qy      184 TTTCAGGACATCANGANGNTGNTGTTTCGATCCCAAGGCGNTCCGTGACAACATATACCAT 243
          |||:::||||:::  |||  :::|||  :::  |||
Db      26 PheArgAspValThrSerLeuLeuGluAspAlaGlnAlaTyrGlnAlaThrIleGlnLeu 45

Qy      244 TTTGTCAAGCGGTACAAGGACCAAGGNATCACCNTGGAAANTAGGAGTTAAAGCTAGAGG 303
          |||:::~::~:|||||||  |||  |||  |||  :::|||||||

```

Db 46 LeuValGluLysTyrLysAspMetGlyPheThrLys-ValValGlyThrGluAlaArgG1 65

QY 304 GNTCANTTTTCGGA 316

Db 65 yPheLeuPheGly 69

# RESULT 10

B90694

adenine phosphoribosyltransferase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)

C;Species: Escherichia coli

C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004

C;Accession: B90694

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Ohtsubo, E.; Nakayama, K.; Murata, T.; Tanaka, M.; Tobe, T.; Iida, T.; Takami, H.; Honda, T.; Sasakawa, C.; Ogasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: B90694

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-183 <HAY>

A;Cross-references: UNIPROT:Q8XD48; GB:BA000007; PIDN:BAB33945.1; PID:g13359979; GSPDB:GN00154

A;Experimental source: strain O157:H7, substrain RIMD 0509952

C;Genetics:

A;Gene: ECs0522

C;Superfamily: adenine phosphoribosyltransferase

## Alignment Scores:

Pred. No.:	2.29e-05	Length:	183
Score:	110.00	Matches:	27
Percent Similarity:	51.39%	Conservative:	10
Best Local Similarity:	37.50%	Mismatches:	34
Query Match:	18.71%	Indels:	1
DB:	2	Gaps:	0

US-09-976-054-5 (1-440) x B90694 (1-183)

QY 103 ATGGCGTNCGCTGATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGAC 162

Db 1 MetThrAlaThrAlaGlnGlnLeuGluTyrLeuLysAsnSerIleLysSerIleGlnAsp 20

QY 163 TTNCCAAAGCCAGGGATNATGTTTCAGGACATCANGANGNTGNTGTTTCGATCCCAAGGCG 222

Db 21 TyrProLysProGlyIleLeuPheArgAspValThrSerLeuLeuGluAspProLysAla 40

QY 223 NTCCGTGACAACATATACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCACCNATGGAA 282

Db 41 TyrAlaLeuSerIleAspLeuLeuValGluArgTyrLysAsnAlaGlyIleAsnLys-Va 60

QY 283 ANTAGGAGTTAAAGCTAGAGGGNTCANTTTTCGGA 316

Db 60 lValGlyThrGluAlaArgGlyPheLeuPheGly 71

RESULT 11

F85544

adenine phosphoribosyltransferase [imported] - Escherichia coli (strain O157:H7, substrain EDL933)

C;Species: Escherichia coli

C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004

C;Accession: F85544

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, G.F.; Evans, P.S.; Gregor, J.; Kirkpatrick, H.A.; Posfai, G.; Hackett, J.; Klink, S.; Boutin, A.; Shao, Y.; Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouisis, K.; Apodaca, J.; Anantharaman, T.S.; Lin, J.; Yen, G.; Schwartz, D.C.; Welch, R.A.; Blattner, F.R.

Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: F85544

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-183 <STO>

A;Cross-references: UNIPROT:Q8XD48; GB:AE005174; NID:g12513339; PIDN:AAG54818.1; GSPDB:GN00145; UWGP:Z0586

A;Experimental source: strain O157:H7, substrain EDL933

C;Genetics:

A;Gene: apt

C;Superfamily: adenine phosphoribosyltransferase

Alignment Scores:

Pred. No.:	2.29e-05	Length:	183
Score:	110.00	Matches:	27
Percent Similarity:	51.39%	Conservative:	10
Best Local Similarity:	37.50%	Mismatches:	34
Query Match:	18.71%	Indels:	1
DB:	2	Gaps:	0

US-09-976-054-5 (1-440) x F85544 (1-183)

Qy	103	ATGGCGTNCGCTGATGCGCGCTTGGCGNGATCGNCTCCTNCATCCNGGTNATNCCCGAC	162
		::    ::	
Db	1	MetThrAlaThrAlaGlnGlnLeuGluTyrLeuLysAsnSerIleLysSerIleGlnAsp	20
Qy	163	TTNCCAAAGCCAGGGATNATGTTTCAGGACATCANGANGNTGNTGTTTCGATCCCAAGGCG	222
		::    ::	
Db	21	TyrProLysProGlyIleLeuPheArgAspValThrSerLeuLeuGluAspProLysAla	40
Qy	223	NTCCGTGACAACATATACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCACCNNTGGAA	282
		::        ::    ::	
Db	41	TyrAlaLeuSerIleAspLeuLeuValGluArgTyrLysAsnAlaGlyIleAsnLys-Va	60
Qy	283	ANTAGGAGTTAAAGCTAGAGGGNTCANTTTTCGGA	316
		::	
Db	60	lValGlyThrGluAlaArgGlyPheLeuPheGly	71

RESULT 12

AD0379

adenine phosphoribosyltransferase (EC 2.4.2.7) [imported] - Yersinia pestis (strain CO92)

C;Species: *Yersinia pestis*  
 C;Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
 C;Accession: AD0379  
 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.;  
 Prentice, M.B.; Sebaihia, M.; James, K.D.; Churcher, C.; Mungall, K.L.; Baker,  
 S.; Basham, D.; Bentley, S.D.; Brooks, K.; Cerdeno-Tarraga, A.M.; Chillingworth,  
 T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Feltwell, T.; Hamlin, N.;  
 Holroyd, S.; Jagels, K.; Leather, S.; Karlyshev, A.V.; Moule, S.; Oyston,  
 P.C.F.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
 Whitehead, S.; Barrell, B.G.  
 Nature 413, 523-527, 2001  
 A;Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.  
 A;Reference number: AB0001; MUID:21470413; PMID:11586360  
 A;Accession: AD0379  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-187 <KUR>  
 A;Cross-references: UNIPROT:Q8ZC94; GB:AL590842; PIDN:CAC92359.1; PID:g15981064;  
 GSPDB:GN00175  
 C;Genetics:  
 A;Gene: apt  
 C;Superfamily: adenine phosphoribosyltransferase  
 C;Keywords: glycosyltransferase; pentosyltransferase

# Alignment Scores:

Pred. No.:	0.000407	Length:	187
Score:	100.00	Matches:	24
Percent Similarity:	48.65%	Conservative:	12
Best Local Similarity:	32.43%	Mismatches:	37
Query Match:	17.01%	Indels:	1
DB:	2	Gaps:	0

US-09-976-054-5 (1-440) x AD0379 (1-187)

Qy	97	GTGGCGATGGCGTNCGCTGATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATN	156
Db	3	ValSerAlaSerLysThrAlaGlnGlnLeuLysTyrIleLysAspSerIleLysThrIle	22
Qy	157	CCCGACTTNCCAAAGCCAGGGATNATGTTTCAGGACATCANGANGNTGNTGTTTCGATCCC	216
Db	23	ProAspTyrProLysAlaGlyIleLeuPheArgAspValThrSerLeuLeuGluAsnPro	42
Qy	217	AAGGCGNTCCGTGACAACATATACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCACC	276
Db	43	LysAlaTyrSerAlaSerIleLysLeuLeuSerGluHisTyrSerGluSerGlyValThr	62
Qy	277	NTGGAAANTAGGAGTTAAAGCTAGAGGGNTCANTTTTCGGA	316
Db	63	Lys-ValValGlyThrGluAlaArgGlyPheLeuPheGly	75

# RESULT 13

G64111  
 adenine phosphoribosyltransferase (EC 2.4.2.7) - *Haemophilus influenzae* (strain Rd KW20)  
 C;Species: *Haemophilus influenzae*  
 C;Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 09-Jul-2004  
 C;Accession: G64111

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.; Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.; FitzHugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton, M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.

A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Accession: G64111

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-180 <TIGR>

A;Cross-references: UNIPROT:P43856; GB:U32802; GB:L42023; NID:g1574151; PIDN:AAC22883.1; PID:g1574160; TIGR:HI1230

C;Genetics:

A;Gene: apt

C;Function:

A;Pathway: purine salvage

C;Superfamily: adenine phosphoribosyltransferase

C;Keywords: glycosyltransferase; pentosyltransferase; salvage pathway

#### Alignment Scores:

Pred. No.:	0.000724	Length:	180
Score:	98.00	Matches:	25
Percent Similarity:	54.55%	Conservative:	11
Best Local Similarity:	37.88%	Mismatches:	29
Query Match:	16.67%	Indels:	1
DB:	2	Gaps:	0

US-09-976-054-5 (1-440) x G64111 (1-180)

```
Qy      121 CGCTTGGCGNGATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAGCCAGGGATN 180
          :::|||      |||      |||      |||      |||:::      |||||      |||
Db      4  GlnLeuAspLeuIleLysSerSerIleLysSerIleProAsnTyrProLysGluGlyIle 23

Qy      181 ATGTTTCAGGACATCANGANGNTGNTGTTTCGATCCCAAGGCGNTCCGTGACAACATATAC 240
          :::|||:::|||||      |||      |||      :::      |||
Db      24  IlePheArgAspIleThrThrLeuLeuGluValProAlaAlaPheLysAlaThrIleAsp 43

Qy      241 CATTTTGTCAAGCGGTACAAGGACCAAGGNATCACCNCTGGAAANTAGGAGTTAAAGCTAG 300
          |||:::~::~|||:::~::~|||~::~|||~::~|||~::~|||      |||      ~::~:~:~|
Db      44  LeuIleValGluGlnTyrArgAspLysGlyIleThrLys-ValLeuGlyThrGluSerAr 63

Qy      301 AGGGNTCANTTTTCGGA 316
          |||      |||||
Db      63  gGlyPheIlePheGly 68
```

#### RESULT 14

F83453

adenine phosphoribosyltransferase PA1543 [imported] - Pseudomonas aeruginosa (strain PA01)

C;Species: Pseudomonas aeruginosa

C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
 C;Accession: F83453  
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Brinkman, F.S.L.; Hufnagle, W.O.; Kowalik, D.J.; Lagrou, M.; Garber, R.L.; Goltry, L.; Tolentino, E.; Westbrook-Wadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, R.M.; Smith, K.A.; Spencer, D.H.; Wong, G.K.S.; Wu, Z.; Paulsen, I.T.; Reizer, J.; Saier, M.H.; Hancock, R.E.W.; Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen.  
 A;Reference number: A82950; MUID:20437337; PMID:10984043  
 A;Accession: F83453  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-182 <STO>  
 A;Cross-references: UNIPROT:Q04633; GB:AE004582; GB:AE004091; NID:g9947492; PIDN:AAG04932.1; GSPDB:GN00131; PASP:PA1543  
 A;Experimental source: strain PA01  
 C;Genetics:  
 A;Gene: apt; PA1543  
 C;Superfamily: adenine phosphoribosyltransferase

Alignment Scores:

Pred. No.:	0.00198	Length:	182
Score:	94.50	Matches:	27
Percent Similarity:	45.45%	Conservative:	13
Best Local Similarity:	30.68%	Mismatches:	46
Query Match:	16.07%	Indels:	2
DB:	2	Gaps:	1

US-09-976-054-5 (1-440) x F83453 (1-182)

Qy	133	ATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAGCCAGGGATNATGTTTCAGGAC	192
		:::                           :::     :::	
Db	8	LeuLysSerGlnIleArgAlaValProAspPheProLysProGlyValValPheArgAsp	27
Qy	193	ATCANGANGNTGNTGTTTCGATCCCAAGGCGNTCCGTGACAACATATACCATTTTGTCAAG	252
		:::         :::       :::	
Db	28	IleThrProLeuPheGlnSerProArgAlaLeuArgMetThrValAspSerPheValGln	47
Qy	253	CGGTACAAGGACCAAGGNATCACCNCTGGAAANTAGGAGTTAAAGCTAGAGGGNTCANTTT	312
		::: ::: :::	
Db	48	ArgTyrIleGluAlaAspPheSerHis-IleGlyAlaMetAspAlaArgGlyPheLeuIle	67
Qy	313	CGGAACAACCTANNTCTTANAANNAATTGGTCAAAAATNGGTGNCNATTGAGGAAGCNA	372
		::: :::	
Db	67	eGlySerAlaValAla---TyrAlaLeuAsnLysProLeuValLeuPheArgLysGlnGln	86
Qy	373	TNAGNTGCCANGCNAAATGATT	394
		::: :::	
Db	86	yLysLeuProAlaAspValLeu	93

RESULT 15  
 RTMSA  
 adenine phosphoribosyltransferase (EC 2.4.2.7) - mouse



N;Alternate names: AMP pyrophosphorylase; gene APRT protein;  
transphosphoribosidase  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 09-Jul-2004  
C;Accession: A22670; I49509  
R;Dush, M.K.; Sikela, J.M.; Khan, S.A.; Tischfield, J.A.; Stambrook, P.J.  
Proc. Natl. Acad. Sci. U.S.A. 82, 2731-2735, 1985  
A;Title: Nucleotide sequence and organization of the mouse adenine  
phosphoribosyltransferase gene: presence of a coding region common to animal and  
bacterial phosphoribosyltransferases that has a variable intron/exon  
arrangement.  
A;Reference number: A22670; MUID:85190571; PMID:3921964  
A;Accession: A22670  
A;Molecule type: DNA  
A;Residues: 1-180 <DUS>  
A;Cross-references: UNIPROT:P08030; GB:M11310; NID:g192009; PIDN:AAA37255.1;  
PID:g387103  
R;Turker, M.S.; Cooper, G.E.; Bishop, P.L.  
J. Mol. Evol. 36, 31-40, 1993  
A;Title: Region-specific rates of molecular evolution: A fourfold reduction in  
the rate of accumulation of silent mutations in transcribed versus  
nontranscribed regions of homologous DNA fragments derived from two closely  
related mouse species.  
A;Reference number: I49509; MUID:93164265; PMID:8433377  
A;Accession: I49509  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 63-107, 'VR', 108-133 <RES>  
A;Cross-references: GB:M86439; NID:g192011; PIDN:AAA37256.1; PID:g553869  
C;Comment: The active enzyme is a dimer of identical chains.  
C;Genetics:  
A;Gene: MGI:Appt  
A;Cross-references: MGI:88061  
A;Introns: 27/2; 63/1; 107/3; 134/1  
C;Superfamily: adenine phosphoribosyltransferase  
C;Keywords: glycosyltransferase; pentosyltransferase; salvage pathway

#### Alignment Scores:

Pred. No.:	0.0352	Length:	180
Score:	84.50	Matches:	23
Percent Similarity:	51.39%	Conservative:	14
Best Local Similarity:	31.94%	Mismatches:	31
Query Match:	14.37%	Indels:	4
DB:	1	Gaps:	1

US-09-976-054-5 (1-440) x RTMSA (1-180)

```

Qy      112 GCTGATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAG 171
          :::::  ||  ::  ||  ||  ||||  ||
Db      2  SerGluProGluLeuLysLeuValAlaArgArgIleArgValPheProAspPheProIle 21

Qy      172 CCAGGGATNATGTTTCAGGACATCANGANGNTGNTGTTTCGATCCCAAGGCGNTCCGTGAC 231
          |||||  ::|||::|||  |||||  ::  ||
Db      22  ProGlyValLeuPheArgAspIleSerProLeuLeuLysAspProAspSerPheArgAla 41

Qy      232 AACATATAACATTTTGTCAAGCGGTACAAGGACCAAGGNATCA-----CCNTGGAA 282
          ::|||  ::|||::||  ::::  ||  ::

```

Db           42 SerIle-ArgLeuLeuAlaSerHisLeuLysSerThrHisSerGlyLysIleAspTyrIl 61  
 Qy           283 ANTAGGAGTTAAAGCTAGAGGGNTCANTTTCGGA 316  
               |||::: .::| |||||       |||||  
 Db           61 eAlaGlyLeuAspSerArgGlyPheLeuPheGly 72

Search completed: December 13, 2004, 21:30:05  
 Job time : 34 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: December 13, 2004, 21:04:50 ; Search time 139 Seconds  
(without alignments)  
3642.660 Million cell updates/sec

Title: US-09-976-054-5  
Perfect score: 588  
Sequence: 1 cgtccgcgcccgcgacttc.....ggaatnntagataaaaaant 440

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 3650362

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+\_n2p.model -DEV=xlp  
-Q=/cgn2\_1/USPTO\_spool\_p/US09976054/runat\_13122004\_160519\_  
24784/app\_query.fasta\_1.583  
-DB=UniProt\_02 -QFMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09976054 @CGN\_1\_1\_244 @runat\_13122004\_160519\_24784 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match Length DB	ID			Description

1	177.5	30.2	243	1	APT1_ARATH	P31166 arabidopsis
2	158.5	27.0	181	2	Q9LW89	Q9lw89 hordeum vul
3	158	26.9	204	2	Q7XJC2	Q7xjc2 brassica na
4	157.5	26.8	181	1	APT1_WHEAT	Q43199 triticum ae
5	156.5	26.6	178	2	Q8H0Y4	Q8h0y4 arabidopsis
6	156.5	26.6	182	2	Q9SU38	Q9su38 arabidopsis
7	153.5	26.1	183	2	Q8LG17	Q8lg17 arabidopsis
8	153.5	26.1	183	2	Q9SUW2	Q9suw2 arabidopsis
9	147.5	25.1	187	2	Q8H534	Q8h534 oryza sativ
10	141.5	24.1	191	2	Q9LFP0	Q9lfp0 arabidopsis
11	141.5	24.1	214	2	Q6RYT6	Q6ryt6 zea mays (m
12	141.5	24.1	214	2	AAR37033	Aar37033 zea mays
13	135.5	23.0	212	2	Q7X6S6	Q7x6s6 oryza sativ
14	135.5	23.0	212	2	Q84P57	Q84p57 oryza sativ
15	135.5	23.0	212	2	CAE02938	Cae02938 oryza sat
16	129.5	22.0	192	1	APT2_ARATH	Q42563 arabidopsis
17	129.5	22.0	192	2	AAL57714	Aal57714 arabidops
18	129.5	22.0	192	2	AAN64513	Aan64513 arabidops
19	126.5	21.5	238	2	Q6K5Y7	Q6k5y7 oryza sativ
20	126.5	21.5	238	2	BAD19719	Bad19719 oryza sat
21	119.5	20.3	213	2	Q6K5Y8	Q6k5y8 oryza sativ
22	119.5	20.3	213	2	BAD19718	Bad19718 oryza sat
23	118	20.1	177	1	APT_LEPIN	Q8exn2 leptospira
24	118	20.1	177	2	Q75FP0	Q75fp0 leptospira
25	118	20.1	177	2	AAS72170	Aas72170 leptospir
26	116.5	19.8	183	1	APT_SHIFL	Q83m42 shigella fl
27	116.5	19.8	183	2	Q7UDH7	Q7udh7 shigella fl
28	116	19.7	183	1	APT_SALTI	Q8z8t4 salmonella
29	116	19.7	183	1	APT_SALTY	Q8zra2 salmonella
30	115	19.6	181	1	APT_VIBVU	Q8db25 vibrio vuln
31	115	19.6	181	1	APT_VIBVY	Q7miv1 vibrio vuln
32	115	19.6	183	1	APT_ECOLI	P07672 escherichia
33	114	19.4	181	1	APT_VIBPA	Q87mq1 vibrio para
34	111.5	19.0	183	1	APT_PHOLL	Q7n0n9 photorhabdu
35	111	18.9	181	1	APT_VIBCH	Q9kt52 vibrio chol
36	110	18.7	183	1	APT_ECO57	Q8xd48 escherichia
37	108	18.4	174	2	Q6LTE9	Q6lte9 photobacter
38	108	18.4	174	2	CAG19427	Cag19427 photobact
39	108	18.4	180	1	APT_PASMU	P57841 pasteurella
40	108	18.4	185	2	Q6D800	Q6d800 erwinia car
41	100	17.0	187	1	APT_YERPE	Q8zc94 yersinia pe
42	98	16.7	171	1	APT_GLOVI	Q7ngz0 gloeobacter
43	98	16.7	180	1	APT_HAEIN	P43856 haemophilus
44	96	16.3	197	1	APT_RALSO	Q8y2b9 ralstonia s
45	94.5	16.1	179	1	APT_HAEDU	Q7vkq4 haemophilus

#### ALIGNMENTS

##### RESULT 1

APT1\_ARATH

ID APT1\_ARATH STANDARD; PRT; 243 AA.

AC P31166; Q8LGF6; Q9FZJ0;

DT 01-JUL-1993 (Rel. 26, Created)

DT 29-MAR-2004 (Rel. 43, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Adenine phosphoribosyltransferase 1 (EC 2.4.2.7) (APRT).  
 GN Name=APT1; Synonyms=APT; OrderedLocusNames=Atlg27450;  
 GN ORFNames=F17L21.24;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=92216042; PubMed=1558943;  
 RA Moffatt B.A., McWhinnie E.A., Burkhart W.E., Pasternak J.J.,  
 RA Rothstein S.J.;  
 RT "A complete cDNA for adenine phosphoribosyltransferase from  
 RT Arabidopsis thaliana.";  
 RL Plant Mol. Biol. 18:653-662(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=94266154; PubMed=8206375;  
 RA Moffatt B.A., McWhinnie E.A., Agarwal S.K., Schaff D.A.;  
 RT "The adenine phosphoribosyltransferase-encoding gene of Arabidopsis  
 RT thaliana.";  
 RL Gene 143:211-216(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=21016719; PubMed=11130712; DOI=10.1038/35048500;  
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,  
 RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,  
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,  
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,  
 RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,  
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,  
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,  
 RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,  
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,  
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,  
 RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,  
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,  
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,  
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,  
 RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,  
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;  
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis  
 RT thaliana.";  
 RL Nature 408:816-820(2000).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305;  
 RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,  
 RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,  
 RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,  
 RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,  
 RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,

RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,  
RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,  
RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,  
RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,  
RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,  
RA Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,  
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;  
RT "Empirical analysis of transcriptional activity in the Arabidopsis  
RT genome.";  
RL Science 302:842-846(2003).  
RN [5]

RP SEQUENCE FROM N.A. (ISOFORM 1).  
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,  
RA Feldmann K.A.;  
RT "Full-length cDNA from Arabidopsis thaliana.";  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Catalyzes a salvage reaction resulting in the formation  
CC of AMP, that is energetically less costly than de novo synthesis.  
CC -!- CATALYTIC ACTIVITY: AMP + diphosphate = adenine + 5-phospho-alpha-  
CC D-ribose 1-diphosphate.  
CC -!- PATHWAY: Purine salvage.  
CC -!- SUBUNIT: Homodimer (By similarity).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=P31166-1; Sequence=Displayed;  
CC Note=No experimental confirmation available;  
CC Name=2;  
CC IsoId=P31166-2; Sequence=VSP\_009002;  
CC -!- SIMILARITY: Belongs to the purine/pyrimidine  
CC phosphoribosyltransferase family.  
CC -!- CAUTION: Ref.3 sequence differs from that shown due to erroneous  
CC gene model prediction.  
CC

-----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC

-----  
DR EMBL; X58640; CAA41497.1; -.  
DR EMBL; L19637; AAA20677.1; -.  
DR EMBL; AC004557; AAF99737.1; ALT\_SEQ.  
DR EMBL; AF325045; AAG40397.1; -.  
DR EMBL; AY128377; AAM91580.1; -.  
DR EMBL; BT000370; AAN15689.1; -.

DR EMBL; AY084300; AAM60891.1; -.  
 DR PIR; S20867; S20867.  
 DR HSSP; P49435; 1G2P.  
 DR InterPro; IPR005764; Ade\_phospho\_trans.  
 DR InterPro; IPR002375; Pr/py\_rp\_transf.  
 DR InterPro; IPR000836; PRtransferase.  
 DR Pfam; PF00156; Pribosyltran; 1.  
 DR TIGRFAMS; TIGR01090; apt; 2.  
 DR PROSITE; PS00103; PUR\_PYR\_PR\_TRANSFER; 1.  
 KW Alternative splicing; Glycosyltransferase; Purine salvage;  
 KW Transferase.  
 FT VARSPLIC 1 60 Missing (in isoform 2).  
 FT /FTId=VSP\_009002.  
 SQ SEQUENCE 243 AA; 26396 MW; 92ABF089CA66C0FD CRC64;

Alignment Scores:

Pred. No.:	2.64e-12	Length:	243
Score:	177.50	Matches:	48
Percent Similarity:	48.46%	Conservative:	15
Best Local Similarity:	36.92%	Mismatches:	51
Query Match:	30.19%	Indels:	16
DB:	1	Gaps:	2

US-09-976-054-5 (1-440) x APT1\_ARATH (1-243)

Qy	49	GCTCCNNTGAGCGTGC	CGCGTCACCGGCGGCAGGCGAGGGCAGGCGGTGGTGGCGATGGCG	108
Db	32	AlaProProSerIleArgLeuSerAsnHisArgSerThrThrSerLeuArgLeuPheSer		51
Qy	109	TNCGCT-----	GATGCGCGCTTG	126
Db	52	SerAlaAlaAlaSerArgAspSerGluMetAlaThrGluAspValGlnAspProArgIle		71
Qy	127	GCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAGCCAGGGATNATGTTT		186
Db	72	AlaLysIleAlaSerSerIleArgValIleProAspPheProLysProGlyIleMetPhe		91
Qy	187	CAGGACATCANGANGNTGNTGTTTCGATCCCAAGGCGNTCCGTGACAACATATACCATTTT		246
Db	92	GlnAspIleThrThrLeuLeuLeuAspThrGluAlaPheLysAspThrIleAlaLeuPhe		111
Qy	247	GTCAAGCGGTACAAGGACCAAGGNATCACCNCTGGAAANTAGGAGTTAAAGCTAGAGGGNT		306
Db	112	ValAspArgTyrLysAspLysGlyIleSerVal-ValAlaGlyValGluAlaArgGlyPh		131
Qy	307	CANTTTTCGGAACAACTANNTCTTANAANNAATTGGTCAAAAATNGGTGNCNATTGAGGAA		366
Db	131	eIlePheGlyProProIleAlaLeuAlaIleGlyAlaLys---PheValProMetArgLy		150
Qy	367	GCNNAATNAGNTGCCANGCNAAATGATT		394
Db	150	sProLysLysLeuProGlyLysValIle		159

RESULT 2

Q9LW89

ID Q9LW89 PRELIMINARY; PRT; 181 AA.

AC Q9LW89;





```

Db      43 ThrThrAspLeuPheValGluArgTyrLysAspLysSerIleThrVal-ValAlaGlyVa 62
QY      292 TAAAGCTAGAGGGNTCANTTTTCGGAACAACCTANNTCTTANAANNAATTGGTCAAAAATNG 351
      |::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      62 lGluAlaArgGlyPheIlePheGlyProProIleAlaLeuAlaIleGlyAlaLys---Ph 81
QY      352 GTGNCNATTGAGGAAGCNAATNAGNTGCCANGCNAAATGATT 394
      :::| | | | | | | | | | | | | | | | | | | | | |
Db      81 eValProIleArgLysProLysLysLeuProGlyGluValIle 95

```

# RESULT 3

Q7XJC2

```

ID      Q7XJC2      PRELIMINARY;      PRT;      204 AA.
AC      Q7XJC2;
DT      01-OCT-2003 (TrEMBLrel. 25, Created)
DT      01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Adenine phosphoribosyltransferase (Fragment).
OS      Brassica napus (Rape).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC      eurosids II; Brassicales; Brassicaceae; Brassica.
OX      NCBI_TaxID=3708;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Ye C.J., Li J., Wang B.;
RL      Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
CC      -!- SIMILARITY: Belongs to the purine/pyrimidine
CC      phosphoribosyltransferase family.
DR      EMBL; AY324112; AAP85303.1; -.
DR      GO; GO:0003999; F:adenine phosphoribosyltransferase activity; IEA.
DR      GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR      GO; GO:0006168; P:adenine salvage; IEA.
DR      GO; GO:0009116; P:nucleoside metabolism; IEA.
DR      InterPro; IPR005764; Ade_phospho_trans.
DR      InterPro; IPR002375; Pr/py_rp_transf.
DR      InterPro; IPR000836; PRtransferase.
DR      Pfam; PF00156; Pribosyltran; 1.
DR      TIGRFAMS; TIGR01090; apt; 1.
DR      PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
KW      Glycosyltransferase; Transferase.
FT      NON_TER      1      1
SQ      SEQUENCE      204 AA; 21800 MW; 587D0F80A7949D4D CRC64;

```

## Alignment Scores:

Pred. No.:	5.81e-10	Length:	204
Score:	158.00	Matches:	44
Percent Similarity:	50.00%	Conservative:	11
Best Local Similarity:	40.00%	Mismatches:	48
Query Match:	26.87%	Indels:	7
DB:	2	Gaps:	2

US-09-976-054-5 (1-440) x Q7XJC2 (1-204)

```

QY      82 CGAGGGCAGGCGGTGGTGGCGATGGCGTNCGCT-----GATGCGCGCTTG 126
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      12 ArgGluSerGluMetAlaAlaAlaAlaAlaAlaLysGluAspGlyGlnAspProArgIle 31

```

Qy 127 GCGGNGATCGNCTCCTNCATCCNGGTNATNCCCCGACTTNCCAAAGCCAGGGATNATGTTT 186  
 Db 32 ProLysIleAlaSerSerIleArgValIleProAspPheProLysProGlyIleMetPhe 51  
 Qy 187 CAGGACATCANGANGNTGNTGTTTCGATCCCAAGGCGNTCCGTGACAACATATACCATTTT 246  
 Db 52 GlnAspIleThrThrLeuLeuLeuAspThrGluAlaPheLysAspThrIleAspIlePhe 71  
 Qy 247 GTCAAGCGGTACAAGGACCAAGGNATCACNTGGAAANTAGGAGTTAAAGCTAGAGGGNT 306  
 Db 72 ValGluArgTyrLysCysLysGlyIleSerVal-ValAlaGlyValGluAlaArgGlyPh 91  
 Qy 307 CANTTTCGGAACAACACTANNTCTTANAANNAATTGGTCAAAAATNGGTGNCNATTGAGGAA 366  
 Db 91 eIlePheGlyProProIleAlaLeuAlaIleGlyAlaLys---PheValProMetArgLy 110  
 Qy 367 GCNNAATNAGNTGCCANGCNAATGATT 394  
 Db 110 sProLysLysLeuProGlyLysValIle 119

#### RESULT 4

APT1\_WHEAT

ID APT1\_WHEAT STANDARD; PRT; 181 AA.

AC Q43199;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DE Adenine phosphoribosyltransferase 1 (EC 2.4.2.7) (APRT).

GN Name=APT1;

OS Triticum aestivum (Wheat).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;

OC Triticeae; Triticum.

OX NCBI\_TaxID=4565;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Capitole; TISSUE=Seed;

RA Moffatt B.A., Schnorr K.S., Gaillard C., Biget E., Laloue M.;

RT "Nucleotide sequence of a wheat cDNA encoding adenine

RT phosphoribosyltransferase.";

RL (er) Plant Gene Register PGR95-030.

CC -!- FUNCTION: Catalyzes a salvage reaction resulting in the formation

CC of AMP, that is energetically less costly than de novo synthesis.

CC -!- CATALYTIC ACTIVITY: AMP + diphosphate = adenine + 5-phospho-alpha-

CC D-ribose 1-diphosphate.

CC -!- PATHWAY: Purine salvage.

CC -!- SUBUNIT: Homodimer (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- SIMILARITY: Belongs to the purine/pyrimidine

CC phosphoribosyltransferase family.

CC

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 CC

DR EMBL; U22442; AAA80609.1; -.  
 DR PIR; T06263; T06263.  
 DR HSSP; P49435; 1G2Q.  
 DR InterPro; IPR005764; Ade\_phospho\_trans.  
 DR InterPro; IPR002375; Pr/py\_rp\_transf.  
 DR InterPro; IPR000836; PRtransferase.  
 DR Pfam; PF00156; Pribosyltran; 1.  
 DR TIGRFAMs; TIGR01090; apt; 1.  
 DR PROSITE; PS00103; PUR\_PYR\_PR\_TRANSFER; 1.  
 KW Glycosyltransferase; Purine salvage; Transferase.  
 SQ SEQUENCE 181 AA; 19664 MW; 3325FBCF3780B24C CRC64;

#### Alignment Scores:

Pred. No.:	6.68e-10	Length:	181
Score:	157.50	Matches:	39
Percent Similarity:	52.63%	Conservative:	11
Best Local Similarity:	41.05%	Mismatches:	43
Query Match:	26.79%	Indels:	2
DB:	1	Gaps:	1

US-09-976-054-5 (1-440) x APT1\_WHEAT (1-181)

Qy	112	GCTGATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAG	171
Db	3	SerAspGlyArgValGluArgIleAlaSerSerIleArgAlaIleProAsnPheProLys	22
Qy	172	CCAGGGATNATGTTTCAGGACATCANGANGNTGNTGTTTCGATCCCAAGGCGNTCCGTGAC	231
Db	23	ProGlyIleLeuPheGlnAspIleThrThrLeuLeuLeuAspProGlnAlaPheArgAsp	42
Qy	232	AACATATAACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCACCNATGGAAANTAGGAGT	291
Db	43	ThrThrAspLeuPheValGluArgTyrLysAspLysAspIleThrVal-ValAlaGlyVa	62
Qy	292	TAAAGCTAGAGGNTCANTTTCGGAACAACCTANNTCTTANAANNAATTGGTCAAAAATNG	351
Db	62	lGluAlaArgGlyPheIlePheGlyProProIleAlaLeuAlaIleGlyAlaLys---Ph	81
Qy	352	GTGNCNATTGAGGAAGCNAATNAGNTGCCANGCNAATGATT	394
Db	81	eValProIleArgLysProLysLysLeuProGlyGluValIle	95

#### RESULT 5

Q8H0Y4

ID Q8H0Y4 PRELIMINARY; PRT; 178 AA.

AC Q8H0Y4;

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DT      01-MAR-2003 (TrEMBLrel. 23, Created)
DT      01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Putative adenine phosphoribosyltransferase.
GN      Name=At4g12440;
OS      Arabidopsis thaliana (Mouse-ear cress).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC      eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX      NCBI_TaxID=3702;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA      Onodera C.S., Quach H.L., Tang C.C., Toriumi M., Wong C., Wu H.C.,
RA      Yu G., Yuan S., Chen H., Cheuk R., Jones T., Kim C.J., Nguyen M.,
RA      Palm C.J., Shinn P., Southwick A., Tripp M.G., Wu T., Davis R.W.,
RA      Ecker J.R., Theologis A.;
RL      Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
CC      -!- SIMILARITY: Belongs to the purine/pyrimidine
CC      phosphoribosyltransferase family.
DR      EMBL; BT001111; AAN64175.1; -.
DR      HSSP; P49435; 1G2P.
DR      GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR      GO; GO:0009116; P:nucleoside metabolism; IEA.
DR      InterPro; IPR002375; Pr/py_rp_transf.
DR      InterPro; IPR000836; PRtransferase.
DR      Pfam; PF00156; Pribosyltran; 1.
DR      PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
KW      Glycosyltransferase; Transferase.
SQ      SEQUENCE 178 AA; 19987 MW; 83E520E5C4EEC8F9 CRC64;

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Alignment Scores:			
Pred. No.:	8.81e-10	Length:	178
Score:	156.50	Matches:	39
Percent Similarity:	53.19%	Conservative:	11
Best Local Similarity:	41.49%	Mismatches:	42
Query Match:	26.62%	Indels:	2
DB:	2	Gaps:	1

Qy	115	GATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCAGACTTNCCAAAGCCA	174
		:::     :::	
Db	8	AspProArgIleAspGlyIleLysThrLysIleArgValValProAspPheProLysLys	27
Qy	175	GGGATNATGTTTTCAGGACATCANGANGNTGNTGTTCGATCCCAAGGCGNTCCGTGACAAC	234
		::	
Db	28	GlyIleMetPheGlnAspIleThrThrLeuLeuLeuAspProLysAlaPheLysAspThr	47
Qy	235	ATATACCATTTTTGTCAAGCGGTACAAGGACCAAGGNATCACNTGGAAANTAGGAGTTAA	294
		:::      :::        :::    ::: ::	
Db	48	IleAspLeuPheValGluArgTyrArgAspMetAsnIleSerVal-ValAlaGlyIleG	67
Qy	295	AGCTAGAGGGNTCANTTTCGGAACAAC TANNCTTANAANNAATTGGTCAAAAATNGGTG	354
		:               ::: ::: -	
Db	67	uAlaArgGlyPheIlePheGlySerProIleAlaLeuAlaIleGlyAlaLys---PheVa	86

Qy 355 NCNATTGAGGAAGCNAATNAGNTGCCANGCNAATGATT 394  
 ||||| ||| ::|||  
 Db 86 lProLeuArgLysProLysLysLeuProGlyGlnIleIle 99

RESULT 6

Q9SU38

ID Q9SU38 PRELIMINARY; PRT; 182 AA.  
 AC Q9SU38;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Putative adenine phosphoribosyltransferase.  
 GN Name=AT4g12440; Synonyms=At4g12440;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hsuan V.W.,  
 RA Lee J.M., Quach H.L., Tang C.C., Toriumi M., Wu H.C., Yu G.,  
 RA Bowser L., Chen H., Cheuk R., Jones T., Karlin-Neumann G., Kim C.,  
 RA Lam B., Lin J., Miranda M., Nguyen M., Palm C.J., Shinn P.,  
 RA Southwick A., Davis R.W., Ecker J.R., Theologis A.;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Peters S.A., van Staveren M., Dirkse W., Stiekema W., Mewes H.W.,  
 RA Lemcke K., Mayer K.F.X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.  
 CC -!- SIMILARITY: Belongs to the purine/pyrimidine  
 CC phosphoribosyltransferase family.  
 DR EMBL; AL049730; CAB41714.1; -.  
 DR EMBL; AY133689; AAM91623.1; -.  
 DR EMBL; AL161534; CAB78287.1; -.  
 DR PIR; T07636; T07636.  
 DR HSSP; P49435; 1G2Q.  
 DR GO; GO:0003999; F:adenine phosphoribosyltransferase activity; IEA.  
 DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.  
 DR GO; GO:0006168; P:adenine salvage; IEA.  
 DR GO; GO:0009116; P:nucleoside metabolism; IEA.  
 DR InterPro; IPR005764; Ade\_phospho\_trans.  
 DR InterPro; IPR002375; Pr/py\_rp\_transf.  
 DR InterPro; IPR000836; PRtransferase.  
 DR Pfam; PF00156; Pribosyltran; 1.  
 DR TIGRFAMs; TIGR01090; apt; 1.  
 DR PROSITE; PS00103; PUR\_PYR\_PR\_TRANSFER; 1.  
 KW Glycosyltransferase; Transferase.  
 SQ SEQUENCE 182 AA; 20355 MW; 976CA5085032935B CRC64;

Alignment Scores:

Pred. No.: 8.81e-10 Length: 182

Score:	156.50	Matches:	39
Percent Similarity:	53.19%	Conservative:	11
Best Local Similarity:	41.49%	Mismatches:	42
Query Match:	26.62%	Indels:	2
DB:	2	Gaps:	1

US-09-976-054-5 (1-440) x Q9SU38 (1-182)

Qy	115	GATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAGCCA	174
Db	8	AspProArgIleAspGlyIleLysThrLysIleArgValValProAspPheProLysLys	27
Qy	175	GGGATNATGTTTTCAGGACATCANGANGNTGNTGTTCGATCCCAAGGCGNTCCGTGACAAC	234
Db	28	GlyIleMetPheGlnAspIleThrThrLeuLeuLeuAspProLysAlaPheLysAspThr	47
Qy	235	ATATACCATTTTTGTCAAGCGGTACAAGGACCAAGGNATCACCN TGAAANTAGGAGTTAA	294
Db	48	IleAspLeuPheValGluArgTyrArgAspMetAsnIleSerVal-ValAlaGlyIleG1	67
Qy	295	AGCTAGAGGGNTCANTTTTCGGAACAAC TANNCTTANAANNAATTGGTCAAAAATNGGTG	354
Db	67	uAlaArgGlyPheIlePheGlySerProIleAlaLeuAlaIleGlyAlaLys---PheVa	86
Qy	355	NCNATTGAGGAAGC NNAATNAGNTGCCANGCNAAATGATT	394
Db	86	lProLeuArgLysProLysLysLeuProGlyGlnIleIle	99

# RESULT 7

Q8LG17

ID	Q8LG17	PRELIMINARY;	PRT;	183 AA.
AC	Q8LG17;			
DT	01-OCT-2002	(TrEMBLrel. 22, Created)		
DT	01-OCT-2002	(TrEMBLrel. 22, Last sequence update)		
DT	01-JUN-2003	(TrEMBLrel. 24, Last annotation update)		
DE	Adenine phosphoribosyltransferase (EC 2.4.2.7)-like protein.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC	eurosids II; Brassicales; Brassicaceae; Arabidopsis.			
OX	NCBI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22088475; PubMed=12093376;			
RA	Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,			
RA	Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;			
RT	"Full-length messenger RNA sequences greatly improve genome			
RT	annotation.";			
RL	Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,			
RA	Feldmann K.;			
RL	Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.			
DR	EMBL; AY084513; AAM61081.1; -.			
DR	HSSP; P49435; 1G2Q.			
DR	GO; GO:0003999; F:adenine phosphoribosyltransferase activity; IEA.			



RA Mayer K.F.X.;  
 RL Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,  
 RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,  
 RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,  
 RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,  
 RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,  
 RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,  
 RA Theologis A.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,  
 RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,  
 RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,  
 RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,  
 RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,  
 RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,  
 RA Theologis A.;  
 RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Wedler H., Wambutt R., Mewes H.W., Lemcke K., Mayer K.F.X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.  
 CC -!- SIMILARITY: Belongs to the purine/pyrimidine  
 CC phosphoribosyltransferase family.  
 DR EMBL; AL033545; CAA22162.1; -.  
 DR EMBL; BT002969; AAO22778.1; -.  
 DR EMBL; BT004412; AAO42406.1; -.  
 DR EMBL; AL161557; CAB79212.1; -.  
 DR PIR; T05451; T05451.  
 DR HSSP; P49435; 1G2Q.  
 DR GO; GO:0003999; F:adenine phosphoribosyltransferase activity; IEA.  
 DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.  
 DR GO; GO:0006168; P:adenine salvage; IEA.  
 DR GO; GO:0009116; P:nucleoside metabolism; IEA.  
 DR InterPro; IPR005764; Ade\_phospho\_trans.  
 DR InterPro; IPR002375; Pr/py\_rp\_transf.  
 DR InterPro; IPR000836; PRtransferase.  
 DR Pfam; PF00156; Pribosyltran; 1.  
 DR TIGRFAMS; TIGR01090; apt; 1.  
 DR PROSITE; PS00103; PUR\_PYR\_PR\_TRANSFER; 1.  
 KW Glycosyltransferase; Transferase.  
 SQ SEQUENCE 183 AA; 20352 MW; F46139F77E31D20B CRC64;

Alignment Scores:

Pred. No.:	2.02e-09	Length:	183
Score:	153.50	Matches:	39
Percent Similarity:	52.13%	Conservative:	10
Best Local Similarity:	41.49%	Mismatches:	43
Query Match:	26.11%	Indels:	2



DB: 2 Gaps: 1

US-09-976-054-5 (1-440) x Q9SUW2 (1-183)

```
Qy      115 GATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAGCCA 174
      ||| |||::: ||| ::: ||| ||| ||||| |||||
Db      9 AspProArgIleHisGlyIleLysThrLysIleArgValValProAspPheProLysLys 28

Qy      175 GGGATNATGTTTCAGGACATCANGANGNTGNTGTTCGATCCCAAGGCGNTCCGTGACAAC 234
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ::|||
Db      29 GlyIleMetPheGlnAspIleThrThrValLeuLeuAspProLysAlaPheLysAspThr 48

Qy      235 ATATACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCACCNCTGGAAANTAGGAGTTAA 294
      ||| |||||:::|||||:::||||::: |||::: |||:::
Db      49 IleAspLeuPheValGluArgTyrArgAspLysAsnIleSerVal-ValAlaGlyIleG1 68

Qy      295 AGCTAGAGGGNTCANTTTCGGAACAACCTANNTCTTANAANNAATTGGTCAAAAATNGGTG 354
      :||||||| ||||| ::: |||
Db      68 uAlaArgGlyPheLeuPheGlyProProIleAlaLeuAlaIleGlyAlaLys---PheVa 87

Qy      355 NCNATTGAGGAAGCNAATNAGNTGCCANGCNAATGATT 394
      ||||| ||| |||
Db      87 lProLeuArgLysProLysLysLeuProGlyGluThrIle 100
```

#### RESULT 9

Q8H534

```
ID Q8H534 PRELIMINARY; PRT; 187 AA.
AC Q8H534;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative adenine phosphoribosyl transferase.
GN Name=OJ1753_E03.106;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: Belongs to the purine/pyrimidine
CC phosphoribosyltransferase family.
DR EMBL; AP003849; BAC81171.1; -.
DR HSSP; P49435; 1G2P.
DR Gramene; Q8H534; -.
DR GO; GO:0003999; F:adenine phosphoribosyltransferase activity; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0006168; P:adenine salvage; IEA.
DR GO; GO:0009116; P:nucleoside metabolism; IEA.
DR InterPro; IPR005764; Ade_phospho_trans.
DR InterPro; IPR002375; Pr/py_rp_transf.
DR InterPro; IPR000836; PRtransferase.
DR Pfam; PF00156; Pribosyltran; 1.
DR TIGRFAMS; TIGR01090; apt; 1.
DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
```

Alignment Scores:

US-09-976-054-5 (1-440) x Q8H534 (1-187)

RESULT 10

09LFP0

ID O9LFP0 PRELIMINARY; PRT; 191 AA.

AC Q9LFP0;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Putative adenine phosphoribosyltransferase.

GN Name=F2I11 50; Synonyms=At5g11160;

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Bevan M., Peters S.A., van Staveren M., Dirkse W., Stiekema W.,

RA Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;

RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA EU Arabidopsis sequencing project;

RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

RN [3]

RP SEQUENCE FROM N.A.  
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,  
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,  
RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,  
RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,  
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,  
RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,  
RA Theologis A.;  
RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,  
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,  
RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,  
RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,  
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,  
RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,  
RA Theologis A.;  
RL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.  
CC -!- SIMILARITY: Belongs to the purine/pyrimidine ,  
CC phosphoribosyltransferase family.  
DR EMBL; AL360314; CAB96651.1; -.  
DR EMBL; BT004028; AAO42064.1; -.  
DR EMBL; BT005077; AAO50610.1; -.  
DR HSSP; P49435; 1G2P.  
DR GO; GO:0003999; F:adenine phosphoribosyltransferase activity; IEA.  
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.  
DR GO; GO:0006168; P:adenine salvage; IEA.  
DR GO; GO:0009116; P:nucleoside metabolism; IEA.  
DR InterPro; IPR005764; Ade\_phospho\_trans.  
DR InterPro; IPR002375; Pr/py\_rp\_transf.  
DR InterPro; IPR000836; PRtransferase.  
DR Pfam; PF00156; Pribosyltran; 1.  
DR TIGRFAMS; TIGR01090; apt; 1.  
DR PROSITE; PS00103; PUR\_PYR\_PR\_TRANSFER; 1.  
KW Glycosyltransferase; Transferase.  
SQ SEQUENCE 191 AA; 20757 MW; EC202C6FBD858E78 CRC64;

Alignment Scores:

Pred. No.:	5.57e-08	Length:	191
Score:	141.50	Matches:	39
Percent Similarity:	50.00%	Conservative:	8
Best Local Similarity:	41.49%	Mismatches:	45
Query Match:	24.06%	Indels:	2
DB:	2	Gaps:	1

US-09-976-054-5 (1-440) x Q9LFP0 (1-191)

Qy	115	GATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAGCCA	174
		:::            :::	
Db	11	AspProArgLeuGluAlaIleSerAlaAlaIleArgValValProAsnPheProLysLys	30
Qy	175	GGGATNATGTTTCAGGACATCANGANGNTGNTGTTTCGATCCCAAGGCGNTCCGTGACAAC	234
		:::	
Db	31	GlyIleMetPheGlnAspIleThrThrLeuLeuLeuAspHisLysAlaPheLysHisThr	50
Qy	235	ATATACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCACCNCTGGAAANTAGGAGTTAA	294

```

      |||      |||||      |||||      |||:::      |||||:::
Db      51 IleAspIlePheValAspArgTyrLysAspMetGlnIleSerVal-ValAlaGlyValG1 70
QY      295 AGCTAGAGGGNTCANTTTCGGAACAACTANNTCTTANAANNAATTGGTCAAAAATNGGTG 354
      :|||      |||||      :::      :|||
Db      70 uAlaArgGlyPheLeuPheGlyProSerIleAlaLeuAlaIleGlyAlaLys---Phe11 89
QY      355 NCNATTGAGGAAGCNNAATNAGNTGCCANGCNAAATGATT 394
      |||||      |||      :::|||
Db      89 eProLeuArgLysProGlyLysLeuProGlyLysValIle 102

```

# RESULT 11

## Q6RYT6

```

ID   Q6RYT6          PRELIMINARY;      PRT;   214 AA.
AC   Q6RYT6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Adenine phosphoribosyltransferase.
GN   Name=apt1;
OS   Zea mays (Maize).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX   NCBI_TaxID=4577;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yu Z., Kong F., Ye C., Liang F., Yang J., Zheng G., Wang B.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the purine/pyrimidine
CC   phosphoribosyltransferase family.
DR   EMBL; AY485263; AAR37033.1; -.
DR   GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR   InterPro; IPR005764; Ade_phospho_trans.
DR   InterPro; IPR002375; Pr/py_rp_transf.
DR   InterPro; IPR000836; PRtransferase.
DR   Pfam; PF00156; Pribosyltran; 1.
DR   TIGRFAMs; TIGR01090; apt; 1.
DR   PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
KW   Glycosyltransferase; Transferase.
SQ   SEQUENCE   214 AA;  22705 MW;  63BA4C4560D0B945 CRC64;

```

## Alignment Scores:

Pred. No.:	5.56e-08	Length:	214
Score:	141.50	Matches:	36
Percent Similarity:	46.32%	Conservative:	8
Best Local Similarity:	37.89%	Mismatches:	49
Query Match:	24.06%	Indels:	2
DB:	2	Gaps:	1

US-09-976-054-5 (1-440) x Q6RYT6 (1-214)

```

QY      100 GCGATGGCGTNCGCTGATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCC 159
      :::::      |||||      |||||      |||      |||      |||
Db      34 SerLeuGlyAlaAlaAspProArgLeuGlnAlaIleSerAspAlaIleArgValValPro 53
QY      160 GACTTNCCAAAGCCAGGGATNATGTTTCAGGACATCANGANGNTGNTGTTTCGATCCCAAG 219

```

```

      ||||| ||||| ||||| |||
Db      54 HisPheProLysProGlyIleMetPheAsnAspIleThrGluLeuLeuLeuArgProGly 73
QY      220 GCGNTCCGTGACAACATATACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCACNTG 279
      ||||| ::: |||||:::|||||::: |||||
Db      74 ValPheArgAspAlaValAspMetPheValGluArgTyrArgGlyMetGlyIleAlaAla 93
QY      280 GAAANTAGGAGTTAAAGCTAGAGGGNTCANTTTCGGAACAACCTANNTCTTANAANNAATT 339
      |||:::||||||| ||||| :::
Db      94 -AlaAlaGlyIleGluAlaArgGlyPheIlePheGlyProAlaIleAlaLeuAlaIleGl 113
QY      340 GGTCAAAAATNGGTGNCNATTGAGGAAGCNNAATNAGNTGCCA 382
      ||| ||||| |||
Db      113 yAlaLys---PheIleProLeuArgLysProLysLysLeuPro 126

```

# RESULT 12

AAR37033

```

ID      AAR37033      PRELIMINARY;      PRT;      214 AA.
AC      AAR37033;
DT      02-MAR-2004 (TrEMBLrel. 27, Created)
DT      02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT      02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE      Adenine phosphoribosyltransferase.
GN      APT1.
OS      Zea mays (Maize).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC      PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX      NCBI_TaxID=4577;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Yu Z., Kong F., Ye C., Liang F., Yang J., Zheng G., Wang B.;
RT      "Cloning and analysis of adenine phosphoribosyltransferase APRT from
RT      maize.";
RL      Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AY485263; AAR37033.1; -.
KW      Glycosyltransferase; Transferase.
SQ      SEQUENCE      214 AA;  22705 MW;  63BA4C4560D0B945 CRC64;

```

## Alignment Scores:

Pred. No.:	5.56e-08	Length:	214
Score:	141.50	Matches:	36
Percent Similarity:	46.32%	Conservative:	8
Best Local Similarity:	37.89%	Mismatches:	49
Query Match:	24.06%	Indels:	2
DB:	2	Gaps:	1

US-09-976-054-5 (1-440) x AAR37033 (1-214)

```

Qy      100 GCGATGGCGTNCGCTGATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCC 159
      ::::: ||||| ||||| ||| ||| ||| |||
Db      34 SerLeuGlyAlaAlaAspProArgLeuGlnAlaIleSerAspAlaIleArgValValPro 53
QY      160 GACTTNCCAAAGCCAGGGATNATGTTTCAGGACATCANGANGNTGNTGTTTCGATCCCAAG 219
      ||||| ||||| ||||| |||
Db      54 HisPheProLysProGlyIleMetPheAsnAspIleThrGluLeuLeuLeuArgProGly 73

```

Qy 220 GCGNTCCGTGACAACATATACCATTTTTGTCAAGCGGTACAAGGACCAAGGNATCACCNTG 279  
 Db 74 ValPheArgAspAlaValAspMetPheValGluArgTyrArgGlyMetGlyIleAlaAla 93  
 Qy 280 GAAANTAGGAGTTAAAGCTAGAGGGNTCANTTTCGGAACAACCTANNTCTTANAANNAATT 339  
 Db 94 -AlaAlaGlyIleGluAlaArgGlyPheIlePheGlyProAlaIleAlaLeuAlaIleGl 113  
 Qy 340 GGTCAAAAATNGGTGNCNATTGAGGAAGCNNAATNAGNTGCCA 382  
 Db 113 yAlaLys---PheIleProLeuArgLysProLysLysLeuPro 126

RESULT 13

Q7X6S6

ID Q7X6S6 PRELIMINARY; PRT; 212 AA.  
 AC Q7X6S6;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE OSJNBa0014K14.10 protein (OSJNBb0116K07.3 protein).  
 GN Name=OSJNBa0014K14.10; Synonyms=OSJNBb0116K07.3;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzeae; Oryza.  
 OX NCBI\_TaxID=39947;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=12447439;  
 RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,  
 RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,  
 RA Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,  
 RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,  
 RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,  
 RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,  
 RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,  
 RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,  
 RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,  
 RA Han B.;  
 RT "Sequence and analysis of rice chromosome 4."  
 RL Nature 420:316-320(2002).  
 CC -!- SIMILARITY: Belongs to the purine/pyrimidine  
 CC phosphoribosyltransferase family.  
 DR EMBL; AL606604; CAE02938.2; -.  
 DR EMBL; AL731638; CAE05550.1; -.  
 DR Gramene; Q7X6S6; -.  
 DR GO; GO:0005622; C:intracellular; IEA.  
 DR GO; GO:0005478; F:intracellular transporter activity; IEA.  
 DR GO; GO:0006888; P:ER to Golgi transport; IEA.  
 DR InterPro; IPR005764; Ade\_phspho\_trans.  
 DR InterPro; IPR002375; Pr/py\_rp\_transf.  
 DR InterPro; IPR000836; PRtransferase.  
 DR Pfam; PF00156; Pribosyltran; 1.  
 DR TIGRFAMs; TIGR01090; apt; 1.  
 DR PROSITE; PS00103; PUR\_PYR\_PR\_TRANSFER; 1.  
 KW Glycosyltransferase; Transferase.  
 SQ SEQUENCE 212 AA; 22708 MW; A30E4A21A8CFB958 CRC64;

# Alignment Scores:

Pred. No.:	2.92e-07	Length:	212
Score:	135.50	Matches:	36
Percent Similarity:	46.32%	Conservative:	8
Best Local Similarity:	37.89%	Mismatches:	49
Query Match:	23.04%	Indels:	2
DB:	2	Gaps:	1

US-09-976-054-5 (1-440) x Q7X6S6 (1-212)

Qy	112	GCTGATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAG	171
Db	36	AlaAspProArgLeuGlnAlaIleSerAspAlaIleArgValValProHisPheProLys	55
Qy	172	CCAGGGATNATGTTTTCAGGACATCANGANGNTGNTGTTTCGATCCCAAGGCGNTCCGTGAC	231
Db	56	ProGlyIleMetPheAsnAspIleThrAlaLeuLeuLeuArgProAlaAlaPheLysAsp	75
Qy	232	AACATATACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCACCNATGGAAANTAGGAGT	291
Db	76	AlaValAspMetPheValGluArgTyrArgGlyMetArgIleAlaAla-ValAlaGlyIle	95
Qy	292	TAAAGCTAGAGGGNTCANTTTCGGAACAACACTANNTCTTANAANNAATTGGTCAAAAATNG	351
Db	95	eGluAlaArgGlyPheIlePheGlyProAlaIleAlaLeuAlaIleGlyAlaLys---Ph	114
Qy	352	GTGNCNATTGAGGAAGCNAATNAGNTGCCANGCNAAATGATT	394
Db	114	eIleProLeuArgLysProLysLysLeuProGlyGluValIle	128

## RESULT 14

Q84P57

ID Q84P57 PRELIMINARY; PRT; 212 AA.  
AC Q84P57;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Adenine phosphoribosyltransferase form 2.  
OS Oryza sativa (indica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=39946;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Li J., Weng M., Wang B.;  
RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.  
CC -!- SIMILARITY: Belongs to the purine/pyrimidine  
CC phosphoribosyltransferase family.  
DR EMBL; AY238894; AA085795.1; -.  
DR HSSP; P49435; 1G2P.  
DR Gramene; Q84P57; -.  
DR GO; GO:0003999; F:adenine phosphoribosyltransferase activity; IEA.  
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.  
DR GO; GO:0006168; P:adenine salvage; IEA.  
DR GO; GO:0009116; P:nucleoside metabolism; IEA.

DR InterPro; IPR005764; Ade\_phospho\_trans.  
 DR InterPro; IPR002375; Pr/py\_rp\_transf.  
 DR InterPro; IPR000836; PRtransferase.  
 DR Pfam; PF00156; Pribosyltran; 1.  
 DR TIGRFAMS; TIGR01090; apt; 1.  
 DR PROSITE; PS00103; PUR\_PYR\_PR\_TRANSFER; 1.  
 KW Glycosyltransferase; Transferase.  
 SQ SEQUENCE 212 AA; 22708 MW; A30E4A21A8CFB958 CRC64;

Alignment Scores:

Pred. No.:	2.92e-07	Length:	212
Score:	135.50	Matches:	36
Percent Similarity:	46.32%	Conservative:	8
Best Local Similarity:	37.89%	Mismatches:	49
Query Match:	23.04%	Indels:	2
DB:	2	Gaps:	1

US-09-976-054-5 (1-440) x Q84P57 (1-212)

QY	112	GCTGATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAG	171
Db	36	AlaAspProArgLeuGlnAlaIleSerAspAlaIleArgValValProHisPheProLys	55
QY	172	CCAGGGATNATGTTTTCAGGACATCANGANGNTGNTGTTTCGATCCCAAGGCGNTCCGTGAC	231
Db	56	ProGlyIleMetPheAsnAspIleThrAlaLeuLeuLeuArgProAlaAlaPheLysAsp	75
QY	232	AACATATACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCACCNCTGGAAANTAGGAGT	291
Db	76	AlaValAspMetPheValGluArgTyrArgGlyMetArgIleAlaAla-ValAlaGlyIle	95
QY	292	TAAAGCTAGAGGGNTCANTTTTCGGAACAACACTANNTCTTANAANNAATTGGTCAAAAATNG	351
Db	95	eGluAlaArgGlyPheIlePheGlyProAlaIleAlaLeuAlaIleGlyAlaLys---Ph	114
QY	352	GTGNCNATTGAGGAAGCNAATNAGNTGCCANGCNAAATGATT	394
Db	114	eIleProLeuArgLysProLysLysLeuProGlyGluValIle	128

RESULT 15

CAE02938

ID CAE02938 PRELIMINARY; PRT; 212 AA.  
 AC CAE02938;  
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
 DE OSJNBa0014K14.10 protein.  
 GN OSJNBa0014K14.10.  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzeae; Oryza; Oryza sativa.  
 OX NCBI\_TaxID=39947;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Nipponbare;  
 RX MEDLINE=22337377; PubMed=12447439;



RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,  
 RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,  
 RA Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,  
 RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,  
 RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,  
 RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,  
 RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,  
 RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,  
 RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,  
 RA Han B.;  
 RT "Sequence and analysis of rice chromosome 4."  
 RL Nature 420:316-320(2002).  
 DR EMBL; AL606604; CAE02938.2; -.  
 SQ SEQUENCE 212 AA; 22708 MW; A30E4A21A8CFB958 CRC64;

Alignment Scores:

Pred. No.:	2.92e-07	Length:	212
Score:	135.50	Matches:	36
Percent Similarity:	46.32%	Conservative:	8
Best Local Similarity:	37.89%	Mismatches:	49
Query Match:	23.04%	Indels:	2
DB:	2	Gaps:	1

US-09-976-054-5 (1-440) x CAE02938 (1-212)

Qy	112	GCTGATGCGCGCTTGGCGGNGATCGNCTCCTNCATCCNGGTNATNCCCGACTTNCCAAAG	171
Db	36	AlaAspProArgLeuGlnAlaIleSerAspAlaIleArgValValProHisPheProLys	55
Qy	172	CCAGGGATNATGTTTCAGGACATCANGANGNTGNTGTTCGATCCCAAGGCGNTCCGTGAC	231
		:::	
Db	56	ProGlyIleMetPheAsnAspIleThrAlaLeuLeuLeuArgProAlaAlaPheLysAsp	75
Qy	232	AACATATAACCATTTTGTCAAGCGGTACAAGGACCAAGGNATCACCNCTGGAAANTAGGAGT	291
		:::      :::     :::        :::	
Db	76	AlaValAspMetPheValGluArgTyrArgGlyMetArgIleAlaAla-ValAlaGlyIl	95
Qy	292	TAAAGCTAGAGGGNTCANTTTTCGGAACAACCTANNTCTTANAANNAATTGGTCAAAAATNG	351
		:::              ::	
Db	95	eGluAlaArgGlyPheIlePheGlyProAlaIleAlaLeuAlaIleGlyAlaLys---Ph	114
Qy	352	GTGNCNATTGAGGAAGCNNAATNAGNTGCCANGCNAAATGATT	394
		::	
Db	114	eIleProLeuArgLysProLysLysLeuProGlyGluValIle	128

Search completed: December 13, 2004, 21:24:19  
 Job time : 143 secs